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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/839,658	04/19/2001	Allan Bradley	11635-004001/ OTA 00-51	9914

7590 01/22/2004

SONIA K. GUTERMAN, ESQ.
MINTZ, LEVIN, COHN, FERRIS, GLOVSKY AND POPEO, P.C
ONE FINANCIAL CENTER
BOSTON, MA 02111

EXAMINER	
STRZELECKA, TERESA E	
ART UNIT	**PAPER NUMBER**
1637	

DATE MAILED: 01/22/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	09/839,658	BRADLEY ET AL.	
	Examiner	Art Unit	
	Teresa E Strzelecka	1637	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *24 September 2003*.

2a)☒ This action is **FINAL**. 2b)☐ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-17,67 and 68* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-17, 67, 68* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. §§ 119 and 120

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

13)☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. § 119(e) (to a provisional application) since a specific reference was included in the first sentence of the specification or in an Application Data Sheet. 37 CFR 1.78.

a) ☐ The translation of the foreign language provisional application has been received.

14)☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. §§ 120 and/or 121 since a specific reference was included in the first sentence of the specification or in an Application Data Sheet. 37 CFR 1.78.

Attachment(s)

1) ☐ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO-1449) Paper No(s) _____ .
4) ☐ Interview Summary (PTO-413) Paper No(s). _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: .

DETAILED ACTION

1. This office action is in response to an amendment filed September 24, 2003. Claims 1-17, 67 and 68 were previously pending. Applicants amended claims 1, 6, 10, 11, 15, 16, 67 and 68. Claims 1-17, 67 and 68 are pending and will be examined.

2. Applicants' amendments overcame the following objections and rejections: objections to claims 1 and 6; rejection of claims 1-14, 17, 67 and 68 under 35 U.S.C. 112, second paragraph. All other rejections are maintained for reasons given in the "Response to Arguments" section below.

Response to Arguments

3. Applicant's arguments filed September 24, 2003 have been fully considered but they are not persuasive.

A) Applicants' arguments regarding rejection of claims 15 and 16 under 35 U.S.C. 112, second paragraph, were considered but were not found persuasive. The terms "substantially an entire chromosome" and "substantially an entire genome" were used in these claims. The reason for the rejection of these two terms as indefinite is that it is not clear what percentage of a chromosome or a genome would be considered as "substantially entire". Would it be 10, 60, 80, 95%?

Applicants argue that "…the term "substantially" with respect to an entire chromosome or genome means that the plurality of immobilized probes contain nucleic acids of a chromosome (or genome) which is almost complete or may be complete, but is not necessarily total, i.e., that "substantially" means almost but possibly not quite all." (page 6 of the Response, second paragraph). However, this hardly clarifies the issue of the metes and bounds of these terms. Applicants further argue that the extent of chromosome (or genome coverage) must be under the control of the user (page 6 of the Response, third paragraph), and therefore 100% coverage is not

necessary in some cases, and "Because of variable needs of users such as customers of a licensee, and variable designs of the nature of the collective set of immobilized nucleic acids that constitute the probe, strict limitations such as 60% of a chromosome or 90% of a genome are not relevant as structural limitations in this art." (page 6 of the Response, fourth paragraph). According to the above arguments, any fragment of genomic DNA or chromosomal DNA would qualify as "substantially entire" genome or chromosome, which, again, leads to the conclusion that the metes and bounds of these claims are not defined.

MPEP 2173.02 cautions

"**MPEP 2173.02**

Examples of claim language which have been held to be indefinite set forth in MPEP § 2173.05(d) are fact specific and should not be applied as per se rules. The test for definiteness under 35 U.S.C. 112, second paragraph is whether "those skilled in the art would understand what is claimed when the claim is read in light of the specification." Orthokinetics, Inc. v. Safety Travel Chairs, Inc., 806 F.2d 1565, 1576, 1 USPQ2d 1081, 1088 (Fed. Cir. 1986)."

The following description is given on page 3, lines 25-31:

"In one embodiment, the target nucleic acid consists essentially of DNA derived from a human. The sample of target genomic nucleic acid can comprise sequences representing a defined fragment of a chromosome or substantially one or more entire chromosomes. The sample of target genomic nucleic acid can comprise sequences representing substantially an entire genome. In an alternative embodiment, the DNA from which the target or the probe nucleic acid is derived from a mammal, such as a mouse or a human genome."

From the above description one cannot conclude what percentage of a chromosome or genome would be considered as "substantially entire". Again, MPEP 2173.02:

MPEP 2173.02

If the language of the claim is such that a person of ordinary skill in the art could not interpret the metes and bounds of the claim so as to understand how to avoid infringement, a rejection of the

claim under 35 U.S.C. 112, second paragraph would be appropriate. See Morton Int 'l, Inc. v. Cardinal Chem. Co., 5 F.3d 1464, 1470, 28 USPQ2d 1190, 1195 (Fed. Cir. 1993).

In the case of these two phrases, one cannot determine metes and bounds of the phrase

"substantially entire", therefore rejection of claims 15 and 16 is maintained.

B) Regarding rejection of claims 1, 2, 6, 7, 12-17, 67 and 68 under 35 U.S.C. 102(b) over

Huang et al., Applicants argue that Applicants' invention of claim 1 does not describe a Southern blot or differential methylation hybridization (DMH) using a CGI library (page 8 of the Response, last paragraph). However, what Applicants claim a method of hybridization of fragmented genomic nucleic acid to an array of nucleic acid probes with each probe at known location, in which method regions of amplification, deletion and unique sequences are detected. Huang et al. teach hybridization of human genomic DNA digested with the restriction enzyme MseI, which generates fragments with lengths ranging from 100-200 base pairs (bp) to an array of 276 CpG island probes, each probe in a known location (Fig. 2; page 468, third paragraph). Therefore, Huang et al. anticipates the limitations of claim 1.

The rejection is maintained.

C) Regarding rejection of claims 1-8, 12, 14-17, 67 and 68 under 35 U.S.C. 102(b) over Cronin et al., Applicants argue that Cronin et al. shows DNA sequence analysis (page 9 of the Response, third paragraph), and that analysis of substantially all human genome by Cronin et al. would require 128,400,000 probes (page 9 of the Response, fourth paragraph). Applicants further argue that the method of Cronin et al. is a method of generating a sequence, not a molecular profile, of a genomic target, and that the method of Cronin et al. is inoperative for an entire genome (page 9 of the Response, last paragraph and page 10, second paragraph).

First, claim 1 is drawn to detection of unique sequences (step c) of claim 1), therefore a method of Cronin et al. of mutation detection by hybridization of genomic DNA to an array of

probes anticipates the limitations of claim 1. The argument about the possible number of probes to analyze the entire genome is irrelevant, since Applicants do not claim any specific size for the array. Further, claim 1 does not include a limitation of analyzing an entire genome or chromosome. Finally, as argued by Applicants with respect to claims 15 and 16, any fragment of genomic DNA can be considered as "substantially entire" genome or chromosome, therefore exon 10 of the CFTR gene would fulfill this definition.

The rejection is maintained.

D) Regarding rejection of claim 9 under 35 U.S.C. 103(a) over Cronin et al. and Waggoner et al., Applicants argue that Waggoner et al. disclose a large number of cyanine dyes, therefore it would not have been obvious to one of ordinary skill in the art to know which one to choose. Applicants further argue that neither Cronin et al. nor Waggoner teach or suggest all of the limitations of claim 1, "… such as providing a plurality of nucleic acid probes comprising a plurality of immobilized nucleic acid segments, which are fragments of genomic nucleic acid, and contacting the probes with fragments of genomic nucleic acid having a length smaller than about 200 bases".

Cronin et al. teach all of the limitations of claim 1, by teaching providing nucleic acid probes comprising a plurality of immobilized nucleic acid segments (Fig. 1), which are fragments of CFTR human genomic DNA (Abstract), and contacting the probes with fragments of genomic DNA having lengths from 20-60 base pairs (page 247, the end of second paragraph), therefore smaller than 200 bp. Thus, Cronin et al. do teach all of the limitations of claim 1. Croni et al. teach labeling the fragments with fluorescein. Waggoner et al. are relied upon to provide the limitation of cyanine dyes. Since the Waggoner et al. patent was published in 1993, by 1996, when the Cronin et al. reference was published, the cyanine dyes were well known. In addition, one of ordinary skill in

the art would have no problem finding out which one of the cyanine dyes to use. Finally, Waggoner et al. provide a very strong motivation for using cyanine dyes:

> "The present invention relates to the labeling with luminescent polymethine cyanine and related polymethine dyes, such as merocyanine and styryl, of proteins and other materials, including nucleic acids, DNA, drugs, toxins, blood cells, microbial materials, particles, plastic or glass surfaces, polymer membranes, etc., at an amine or hydroxy site on those materials. The dyes are advantageously soluble in aqueous or other medium in which the labeled material is contained."

(col. 2, lines 58-64) and

> "The cyanine and related dyes of this invention are especially well adapted for the analysis of a mixture of components wherein dyes of a variety of excitation and emission wavelengths are required because specific cyanine and related dyes can be synthesized having a wide range of excitation and emission wavelengths. Specific cyanine and related dyes having specific excitation and emission wavelengths can be synthesized by varying the number of methine groups or by modifying the cyanine ring structures. In this manner, it is possible to synthesize dyes having particular excitation wavelengths to correspond to a particular excitation light source, such as a laser, e.g., a HeNe laser or a diode laser."

(col. 4, lines 36-49).

As the method of Cronin et al. is drawn to detection of multiple mutations, one of skill in the art would be motivated to use cyanine dyes for this purpose.

The rejection is maintained.

E) Regarding rejection of claim 10 under 35 U.S.C. 103(a) over Cronin et al. and Anderson et al., Applicants argue that lane F of Anderson's Fig. 1 show no visible band in the size range shorter than 200 bp, and that by teaching pooling fractions of DNA fragments with sizes from 300

to 1000 base pairs, Anderson et al. teach away from sizes smaller than 200 bases. Further, Applicants argue that Cronin et al. does not teach DNA fragmentation by DNAse digestion.

As to the Fig. 1 of Anderson, another copy of the paper is provided, in which a band with size smaller than the 141 bp fragment is clearly visible. Cronin et al. do teach fragmentation of DNA by enzymatic digestion, since they teach digestion of genomic DNA with uracil-N-glycosylase (page 247, the end of second paragraph). What Anderson et al. show is that fragmentation in a desired size range can be obtained by adjusting DNAse concentration (Fig. 1). Further, the motivation provided by Anderson et al. points to the clear advantage of using DNAse over other enzymes, such as restriction enzymes: "The average size of the resultant fragments were found to be inversely proportional to the amount of enzyme in the digest and the distributions were smooth and unimodal (Fig. 1). This indicated that there were no obvious preferentially digested or resistant sequences present in the digest." (page 3019, first paragraph). Therefore, one of skill in the art would be motivated to use DNAse fractionation of genomic DNA over the fractionation method of Cronin et al., which requires pre-amplification of genomic DNA in the presence of dUTP.

The rejection is maintained.

F) Regarding rejection of claim 11 under 35 U.S.C. 103(a) over Cronin et al., Anderson et al. and Ordahl et al., Applicants argue that Cronin et al., Anderson et al. and Ordahl et al. do not teach limitations of claim 1. Applicants further argue that Cronin et al. uses photolitographically synthesized polynucleotides with predetermined sequences to make an array, therefore art of Cronin et al. is different from the art of Anderson et al. and Ordahl et al. Finally, Applicants argue that there is no motivation to combine theses references.

Regarding the argument that Cronin et al. do not teach limitations of claim 1, the argument was addressed in part D) of this response. Further, the fact that Cronin et al. teaches an array and Anderson et al. and Ordahl et al. do not, is irrelevant. Cronin et al. teach fragmentation of genomic DNA by enzymatic digest, Anderson et al. teach fragmentation of DNA by enzymatic digest, and Ordahl et al. teach fragmentation of DNA by shearing. The motivation to combine Anderson et al. and Cronin et al. was reiterated in part E) of this response. The motivation to use fragmentation, as provided by Ordahl et al., was that in hybridization experiments "… on kinetic and other grounds it is advantageous to use short DNA fragments less than 500 base pairs in length. This length not only permits separation of the repetitive and nonrepetitive components of most eucaryotic genomes, but also reduces the amount of single strand tails in reassociated and hybrid duplexes" (page 2985, first paragraph). Therefore, both Anderson et al. and Ordahl et al. provide ample motivation to combine with Cronin et al.

The rejection is maintained.

Claim Rejections - 35 USC § 112

4. The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

5. Claims 15 and 16 rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

A) Claim 15 is indefinite over the recitation of "substantially an entire chromosome". It is not clear what percentage of the total chromosome would be considered as "substantially entire", and the specification does not provide a definition or examples.

B) Claim 16 is indefinite over the recitation of "substantially an entire genome". It is not clear what percentage of the total genome would be considered as "substantially entire", and the specification does not provide a definition or examples.

Claim Rejections - 35 USC § 102

6. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

7. Claims 1, 2, 6, 7, 12-17, 67 and 68 are rejected under 35 U.S.C. 102(b) as being anticipated by Huang et al. (Human Mol. Genetics, vol. 8, pp. 459-470, March 1999; cited in the IDS; cited in the previous office action).

Regarding claims 1, 2, 6, 7, 14-17, 67 and 68, Huang et al. teach profiling of a methylation pattern of genomic DNA in breast cancer cells. Genomic DNA from six human breast cancer cell lines was digested with the restriction enzyme MseI, which generates fragments with lengths ranging from 100-200 base pairs (bp). The fragments were ligated to linkers, treated with BstUI restriction enzyme and amplified. The amplified DNA fragments were labeled with ^{32}P. (Fig. 2; page 460, second and third paragraphs; page 468, second paragraph).

The amplified DNA fragments were then hybridized to an array of 276 CpG island probes (Fig. 2; page 468, third paragraph).

Regarding claim 12 and 13, Huang et al. teach stringent hybridization conditions at a temperature of 65° C (page 468, third paragraph).

8. Claims 1-8, 12, 14-17, 67 and 68 are rejected under 35 U.S.C. 102(b) as being anticipated by Cronin et al. (Human Mutation, vol. 7, pp. 244-255, 1996; cited in the previous office action).

Regarding claims 1-8, Cronin et al. teach detection of cystic fibrosis mutations by hybridization of target nucleic acids to an array of immobilized probes. Two types of arrays were used: one had probes which allowed identification of differences from the wild type sequences in exon 11, the second array contained 1480 probes for detection of deletions, insertions and base substitutions (Abstract; page 245, 246). Genomic DNA used in the hybridization experiments was amplified, labeled with fluorescein by amplification with fluorescein-labeled nucleotides, then the amplification products were fragmented with uracil-N-glycosylase. The fragmented PCR products were 20-60 bp long. The labeled, fragmented Target DNA was hybridized with the arrays, and the images were obtained using a confocal epifluorescent microscope (page 247).

Regarding claim 12, Cronin et al. teach stringent hybridization conditions (page 245, second column).

Regarding claims 14-17, 67 and 68, Cronin et al. teach genomic samples obtained from human CFTR patients (page 247, first paragraph).

Claim Rejections - 35 USC § 103

9. The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

10. Claim 9 is rejected under 35 U.S.C. 103(a) as being unpatentable over Cronin et al. as applied to claim 8 above, and further in view of Waggoner et al. (U. S. Patent No. 5,268,486; cited in the previous office action).

A) Claim 9 is drawn to the label comprising Cy3 or Cy5.

B) Cronin et al. teach fluorescent labels, but do not teach Cy3 or Cy5.

C) Waggoner et al. teach luminescent cyanine dyes, including Cy3 and Cy 5 (col. 19, formula at the bottom; claim 8; Cy3 has m=1, Cy5 has m=2). the dyes can be used to label nucleic acids (col. 2, lines 58-61; col. 4, lines 29-35).

It would have been *prima facie* obvious to one of ordinary skill in the art at the time of the invention to have used the cyanine dyes of Waggoner et al. in the method of Cronin et al. The motivation to do so, provided by Waggoner et al., would have been that cyanine dyes were used for detecting mixtures of components because they had a wide range of excitation and emission wavelengths (col. 4, lines 36-49).

11. Claim 10 is rejected under 35 U.S.C. 103(a) as being unpatentable over Cronin et al. as applied to claim 1 above, and further in view of Anderson (Nucl. Acids Res., vol. 9, pp. 3015-3027, 1981; cited in the previous office action).

A) Claim 10 is drawn to fragmentation of genomic DNA to sizes smaller than 200 bases by DNAse digestion.

B) Cronin et al. do not teach fragmentation of DNA by DNAse digestion.

C) Anderson teaches fragmentation of genomic DNA to sizes below 200 base pairs by digestion with 2.2 ng or more of DNAse I (Figure 1).

It would have been *prima facie* obvious to one of ordinary skill in the art at the time of the invention to have used DNAse I digestion of Anderson to fragment genomic target DNA in the method of Cronin et al. The motivation to do so, provided by Anderson, would have been that DNAse I digestion was sequence-independent and the sizes distribution obtained could be regulated by regulating the amount of DNAse I in the reaction (page 3019, first two paragraphs).

12. Claim 11 is rejected under 35 U.S.C. 103(a) as being unpatentable over Cronin et al. as applied to claim 1 above, and further in view of Ordahl et al. (Nucl. Acids Res., vol. 3, pp. 2985-

2999, 1976; cited in the previous office action) and Anderson (Nucl. Acids Res., vol. 9, pp. 3015-3027, 1981; cited in the previous office action).

A) Claim 11 is drawn to fragmentation of genomic DNA to sizes smaller than 200 bases by applying shear forces to fragment genomic DNA followed DNAse digestion.

B) Cronin et al. do not teach fragmentation of genomic DNA to sizes smaller than 200 bases by applying shear forces to fragment genomic DNA followed DNAse digestion.

C) Ordahl et al. teach fragmentation of genomic DNA in preparation for DNA hybridization experiments. Ordahl et al. teach that it is advantageous to use DNA fragments of less than 500 bp in hybridization experiments (page 2985, first paragraph). Ordahl et al. teach that DNA fragmented in French press had an average size of 230 base pairs (Abstract; page 2986; Fig. 4). Ordahl et al. do not teach DNAse I fragmentation after shearing.

D) Anderson teaches fragmentation of genomic DNA to sizes below 200 base pairs by digestion with 2.2 ng or more of DNAse I (Figure 1).

It would have been *prima facie* obvious to one of ordinary skill in the art at the time of the invention to have used shearing of Ordahl et al. and DNAse I digestion of Anderson to fragment genomic target DNA in the method of Cronin et al. The motivation to do so, provided by Ordahl et al. and Anderson, would have been that it was advantageous to use short DNA fragments in hybridization (Ordahl, p. 2885, first paragraph) and that DNAse I digestion was sequence-independent and the sizes distribution obtained could be regulated by regulating the amount of DNAse I in the reaction (Anderson, page 3019, first two paragraphs).

13. Claim 13 rejected under 35 U.S.C. 103(a) as being unpatentable over Cronin et al. as applied to claim 12 above, and further in view of Anderson et al. ("Nucleic acid hybridization, a practical approach", IRL Press, Oxford-Washington DC, pp. 93-95, 1985; cited in the previous office action).

A) Claim 13 is drawn to the stringent hybridization conditions comprising a temperature of about 60-65° C.

B) Cronin et al. teach stringent hybridization conditions of incubation at 30° C and washing at 25-30° C for probes which are 15 bp long (page 247, second column, first paragraph). Cronin et al. do not teach a temperature of 60 to 65° C.

C) Anderson et al. teach that temperature and salt concentration of the washing solution determine which hybrids will be dissociated, and is usually chosen to be at 5-20° C below Tm for well-matched hybrids (page 95, first paragraph). Therefore the wash temperature will depend on the probe's length, GC content and ionic strength of the solution, since Tm depends on these variables.

It would have been *prima facie* obvious to one of ordinary skill in the art to adjust the temperature of the stringent wash solution according to Anderson et al. when considering probes of different lengths and compositions than the probes used by Cronin et al. The motivation to do would have been that adjusting hybridization conditions allowed discrimination between matched and mismatched probe-target complexes.

14. No claims are allowed.

Conclusion

15. **THIS ACTION IS MADE FINAL.** Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the

date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the mailing date of this final action.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Teresa E Strzelecka whose telephone number is (571) 272-0789. The examiner can normally be reached on M-F (8:30-5:30).

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Gary Benzion can be reached on (703) 308-1119. The fax phone number for the organization where this application or proceeding is assigned is (703) 872-9306.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is (703) 308-0196.

Gary Benzion will move to the new office on January 22, 2004. His new phone number is (571) 272-0782.

JEFFREY FREDMAN
PRIMARY EXAMINER

TS
January 14, 2004